



SEQUENCE LISTING

<110> ENDO, NOBORU
YOSHIDA, KOUKI
AKIYOSHI, MIHO
YOSHIDA, YASUKO
OHSUMI, CHIEKO
IGARASHI, DAISUKE

<120> GENE CAPABLE OF IMPARTING SALT STRESS RESISTANCE

<130> 279689US0XPCT

<140> 10/553,124

<141> 2005-10-14

<150> PCT/JP04/05403

<151> 2004-04-15

<150> JP 2003-113194

<151> 2003-04-17

<150> JP 2004-075932

<151> 2004-03-17

<160> 20

<170> PatentIn version 3.3

<210> 1

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<213> Seashore Paspalum

<220>

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<222> (131) .. (1222)

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gacggcgcag atg gcg atc ggc ggg gcg gag gcc ggc ggg gga ggc gcg 169

Met Ala Ile Gly Gly Ala Glu Ala Gly Gly Gly Gly Ala

1

5

10

ggg gcc agc ggc cgg agc gtg ctg gtg acg ggc ggc gcg ggg ttc atc 217

Gly Ala Ser Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile

15

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gtc Val	gtc Val	gac Asp	aac Asn	ttc Phe 50	cac His	aac Asn	tcc Ser	gtc Val	ccc Pro 55	gag Glu	gcg Ala	ctc Leu	gaa Glu	cgc Arg 60	gtc Val	313
cgc Arg	ctc Leu	atc Ile	gcc Ala 65	ggg Gly	ccc Pro	gcg Ala	ctc Leu	tcc Ser 70	gcc Ala	cgc Arg	ctc Leu	gac Asp	ttc Phe 75	atc Ile	cgg Arg	361
ggg Gly	gat Asp	ctg Leu 80	agg Arg	agc Ser	gcc Ala	ggg Gly	gac Asp 85	ttg Leu	gag Glu	aag Lys	gcg Ala	ttc Phe 90	gcg Ala	gcc Ala	agg Arg	409
agg Arg	tac Tyr 95	gac Asp	gcc Ala	gtc Val	gtc Val	cac His 100	ttc Phe	gcg Ala	ggg Gly	ctc Leu	aag Lys 105	gcc Ala	gtc Val	ggg Gly	gag Glu	457
agc Ser 110	gtc Val	gcg Ala	cgc Arg	ccg Pro	gac Asp 115	atg Met	tac Tyr	tac Tyr	gag Glu	aac Asn 120	aac Asn	ctc Leu	gcc Ala	ggc Gly	acc Thr 125	505
atc Ile	aac Asn	ctc Leu	tac Tyr	aag Lys 130	gcc Ala	atg Met	aac Asn	gag Glu	cac His 135	ggc Gly	tgc Cys	aag Lys	aag Lys	atg Met 140	gtg Val	553
ttc Phe	tcg Ser	tcg Ser	tcc Ser 145	gcg Ala	acc Thr	gtg Val	tac Tyr	ggc Gly 150	tgg Trp	ccg Pro	gag Glu	gtg Val	atc Ile 155	ccg Pro	tgc Cys	601
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ctc Leu 175	atc Ile	ctg Leu	gag Glu	gag Glu	ttg Leu	gcg Ala 180	cgg Arg	gac Asp	tac Tyr	cag Gln	cgc Arg 185	gcg Ala	gac Asp	ccg Pro	ggc Gly	697
tgg Trp 190	agc Ser	atc Ile	gtc Val	ctg Leu	ctg Leu 195	cgc Arg	tac Tyr	ttc Phe	aac Asn	ccc Pro 200	atc Ile	ggc Gly	gcc Ala	cac His	agc Ser 205	745
tcc Ser	ggc Gly	gag Glu	atc Ile	ggc Gly 210	gag Glu	gac Asp	ccc Pro	aag Lys	ggg Gly 215	gtg Val	ccc Pro	aac Asn	aac Asn	ctg Leu 220	ctg Leu	793
ccc Pro	tac Tyr	atc Ile	cag Gln	cag Gln	gtc Val	gcc Ala	gtc Val	ggc Gly	agg Arg	ctc Leu	ccc Pro	gag Glu	ctc Leu	aac Asn	gtc Val	841

225				230				235				
tac ggc cac gat	tac ccc acc cgt	gac ggc acc gcg	atc agg gac tac	889								
Tyr Gly His Asp	Tyr Pro Thr Arg	Asp Gly Thr Ala	Ile Arg Asp Tyr									
240	245	250										
ata cac gtc gtc	gac ctg gcc gac	ggg cac atc gcg	gcg ctg aac aag	937								
Ile His Val Val	Asp Leu Ala Asp	Gly His Ile Ala	Ala Ala Leu Asn Lys									
255	260	265										
ctg ttc gac act	cct gat ttc ggt	tgt gtg gcc tac	aat ctg ggc aca	985								
Leu Phe Asp Thr	Pro Asp Phe Gly	Cys Val Ala Tyr	Asn Leu Gly Thr									
270	275	280	285									
ggg cgc ggc aca	tcc gtt ctc gag	atg gtg gcg gcg	ttc aag aag gca	1033								
Gly Arg Gly Thr	Ser Val Leu Glu	Met Val Ala Ala	Phe Lys Lys Ala									
290	295	300										
tcc ggc aag gag	atc ccc acc aag	atg tgc ccc agg	aga ccg ggt gac	1081								
Ser Gly Lys Glu	Ile Pro Thr Lys	Met Cys Pro Arg	Arg Pro Gly Asp									
305	310	315										
gcg acg gag gtt	tac gcg tcc act	gag aag gcc gaa	agg gag ctc gga	1129								
Ala Thr Glu Val	Tyr Ala Ser Thr	Glu Lys Ala Glu	Arg Glu Leu Gly									
320	325	330										
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Trp Arg Ala Gln	Tyr Gly Ile Glu	Glu Met Cys Arg	Asp Gln Trp Asn									
335	340	345										
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350	355	360										
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 <212> PRT
 <213> Seashore Paspalum

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Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr Val Val Asp
35 40 45

Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val Arg Leu Ile
50 55 60

Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg Gly Asp Leu
65 70 75 80

Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg Arg Tyr Asp
85 90 95

Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala
100 105 110

Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr Ile Asn Leu
115 120 125

Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val Phe Ser Ser
130 135 140

Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys Val Glu Asp
145 150 155 160

Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile Leu
165 170 175

Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly Trp Ser Ile
180 185 190

Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser Ser Gly Glu
195 200 205

Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr Ile
210 215 220

Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val Tyr Gly His
225 230 235 240

Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr Ile His Val
245 250 255

Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys Leu Phe Asp
260 265 270

Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg Gly
275 280 285

Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala Ser Gly Lys
290 295 300

Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp Ala Thr Glu
305 310 315 320

Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly Trp Arg Ala
325 330 335

Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Lys
340 345 350

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355 360

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atctccatct cccacccccca tcgatccatt tgtgttggct ttaattccct gcgtgcatgc 180
gtgttggtga ataagggggcc ggttccatct gtacgtacgt gtactccgag acctatcgtc 240
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ctcagaccta tcggtggaag atgtaacaag tagagaccgc tcgaatgtgc ctagctacga 180

agtttcgtac catctctctt gtcataacct catgtagatg gtcattttat tggaattagc 240
 cttagccttc aggccccggcg ctgttaaaat ttgtttttaca catggatttt ctcgctacgt 300
 gtgatacata ttgtgtctgt aataatcctg atcggagttt ccagtaataa aaccgatcca 360
 cgacggtggc tacgccctgt gttgtagtac tgtgaatatg atgtggtaat aacaataact 420
 tgcagtgaga cttcagcttt caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 480
 aaaaaaaaaa aaaaaaa 497

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 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

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 ctgccgaaaa atagagcgcg tgcattaatc agatctctgg actgaatttg tccatgggtg 120
 atggttgtct cagacctatc ggtggaagat gtaacaagta gagaccgctc gaatgtgcct 180
 agctacgaag ttctgtacca tctctcttgt cataacctca tgtagatggc cattttattg 240
 gaattagcct tagccttcag gcccggcgct gttaaaattt gttttacaca tggattttct 300
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Met Val Ser																
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gcg	gtg	ctt	cgt	acc	atc	ctt	gtg	acg	ggc	ggc	gcc	ggc	tac	atc	ggc	166
Ala	Val	Leu	Arg	Thr	Ile	Leu	Val	Thr	Gly	Gly	Ala	Gly	Tyr	Ile	Gly	
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agc	cac	acc	gtg	ctg	ctg	ctg	ctg	cag	cag	gga	ttc	cgc	gtc	gtc	gtc	214
Ser	His	Thr	Val	Leu	Leu	Leu	Leu	Gln	Gln	Gly	Phe	Arg	Val	Val	Val	
20				25						30					35	
gtc	gac	aac	ctc	gac	aac	gcc	tcc	gac	gtc	gcg	ctc	gcc	cgc	gtc	gcg	262
Val	Asp	Asn	Leu	Asp	Asn	Ala	Ser	Asp	Val	Ala	Leu	Ala	Arg	Val	Ala	
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cag	ctc	gca	gca	agc	agc	aac	ggc	ggc	gcc	gcc	aac	ctc	gtc	ttc	cac	310
Gln	Leu	Ala	Ala	Ser	Ser	Asn	Gly	Gly	Ala	Ala	Asn	Leu	Val	Phe	His	
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aag	gtt	gac	ctt	cgc	gac	agg	cac	gcg	ctg	gag	gac	atc	ttc	tcc	tcc	358
Lys	Val	Asp	Leu	Arg	Asp	Arg	His	Ala	Leu	Glu	Asp	Ile	Phe	Ser	Ser	
		70					75					80				
cac	agg	ttt	gag	gct	gtg	att	cat	ttt	gct	ggg	ctc	aaa	gct	gtt	ggc	406
His	Arg	Phe	Glu	Ala	Val	Ile	His	Phe	Ala	Gly	Leu	Lys	Ala	Val	Gly	
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gag	agc	gtg	cag	aag	ccg	ctg	ctt	tac	tac	gac	aac	aac	ctc	atc	ggc	454
Glu	Ser	Val	Gln	Lys	Pro	Leu	Leu	Tyr	Tyr	Asp	Asn	Asn	Leu	Ile	Gly	
100					105					110					115	
acc	atc	acc	ctc	ctc	gag	gtc	atg	gcc	gca	cat	ggc	tgc	aag	aag	ctg	502
Thr	Ile	Thr	Leu	Leu	Glu	Val	Met	Ala	Ala	His	Gly	Cys	Lys	Lys	Leu	
				120					125					130		
gtg	ttc	tcg	tca	tct	gca	act	gtc	tat	ggg	tgg	ccc	aag	gaa	gtg	cca	550
Val	Phe	Ser	Ser	Ser	Ala	Thr	Val	Tyr	Gly	Trp	Pro	Lys	Glu	Val	Pro	
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tgc	acc	gaa	gaa	ttc	cct	ctt	tgc	gcc	acc	aac	ccc	tat	ggg	cga	acc	598
Cys	Thr	Glu	Glu	Phe	Pro	Leu	Cys	Ala	Thr	Asn	Pro	Tyr	Gly	Arg	Thr	
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aag	ctt	gtg	att	gaa	gat	atc	tgc	cgc	gac	gtc	cac	cgt	tca	gac	cct	646
Lys	Leu	Val	Ile	Glu	Asp	Ile	Cys	Arg	Asp	Val	His	Arg	Ser	Asp	Pro	
	165					170					175					
gat	tgg	aag	atc	ata	ctg	ctc	agg	tac	ttc	aac	cct	gtt	ggg	gct	cat	694
Asp	Trp	Lys	Ile	Ile	Leu	Leu	Arg	Tyr	Phe	Asn	Pro	Val	Gly	Ala	His	
180					185					190					195	

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Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro Asn Asn Leu	
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atg ccc tat gtc cag caa gtt gcc gtt ggg agg agg cct cac ctc act	790
Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro His Leu Thr	
215 220 225	
gtc tat gga acc gac tac aac aca aag gat gga act ggg gtg cgc gat	838
Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly Val Arg Asp	
230 235 240	
tat atc cat gtt gtt gac ctg gcc gat ggg cac ata gca gcc ctg ggg	886
Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Gly	
245 250 255	
aag ctc tat gaa gac tct gac aga ata ggg tgt gag gta tac aac ctg	934
Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val Tyr Asn Leu	
260 265 270 275	
ggc aca gga aag ggg act tcg gtg ctg gaa atg gtg gct gca ttc gag	982
Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu	
280 285 290	
aag gtt tct ggc aag aaa atc cct ctg gtg ctt gct ggg cga aga cct	1030
Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly Arg Arg Pro	
295 300 305	
gga gat gca gag att gtt tat gct gca act gcc aag gcc gag aaa gag	1078
Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala Glu Lys Glu	
310 315 320	
ctg aaa tgg aag gcc aag tac ggg att gaa gag atg tgc aga gac cag	1126
Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln	
325 330 335	
tgg aac tgg gca agc aaa aac ccc tac ggg tat gct gga tca ccc gac	1174
Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly Ser Pro Asp	
340 345 350 355	
aac agc agc tgactgaaag caaatgcatg ctatgcatga tagggagatc	1223
Asn Ser Ser	
gagcagcaga ccacttacca ctgctagtaa aagaagtcga gtctcagaat accaccgtac	1283
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ttctcatttg tatagaggga cggagtagga gateccccagt cccatccatc cggcttattg	1403
ttgctaccgt caatccatgt ttaagaaata aaccctatg catgtatgct tatcgatcta	1463

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 aaaaaaaaaa aaaaaaa 1540

<210> 9
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 <212> PRT
 <213> Seashore Paspalum

<400> 9

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 35 40 45

Arg Val Ala Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu
 50 55 60

Val Phe His Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile
 65 70 75 80

Phe Ser Ser His Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys
 85 90 95

Ala Val Gly Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn
 100 105 110

Leu Ile Gly Thr Ile Thr Leu Leu Glu Val Met Ala Ala His Gly Cys
 115 120 125

Lys Lys Leu Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys
 130 135 140

Glu Val Pro Cys Thr Glu Glu Phe Pro Leu Cys Ala Thr Asn Pro Tyr
 145 150 155 160

Gly Arg Thr Lys Leu Val Ile Glu Asp Ile Cys Arg Asp Val His Arg
165 170 175

Ser Asp Pro Asp Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val
180 185 190

Gly Ala His Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro
195 200 205

Asn Asn Leu Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro
210 215 220

His Leu Thr Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly
225 230 235 240

Val Arg Asp Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala
245 250 255

Ala Leu Gly Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val
260 265 270

Tyr Asn Leu Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala
275 280 285

Ala Phe Glu Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly
290 295 300

Arg Arg Pro Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala
305 310 315 320

Glu Lys Glu Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys
325 330 335

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340 345 350

Ser Pro Asp Asn Ser Ser

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27

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cgaacccgct cgtctggcta

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<210> 18
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<212> PRT

<213> Arabidopsis thaliana

<400> 18

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Val Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Ile Glu Ala Val Asp
35 40 45

Arg Val Arg Glu Leu Val Gly Pro Asp Leu Ser Lys Lys Leu Asp Phe
50 55 60

Asn Leu Gly Asp Leu Arg Asn Lys Gly Asp Ile Glu Lys Leu Phe Ser
65 70 75 80

Lys Gln Arg Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val
85 90 95

Gly Glu Ser Val Glu Asn Pro Arg Arg Tyr Phe Asp Asn Asn Leu Val
100 105 110

Gly Thr Ile Asn Leu Tyr Glu Thr Met Ala Lys Tyr Asn Cys Lys Met
115 120 125

Met Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Ile
130 135 140

Pro Cys Met Glu Asp Phe Glu Leu Lys Ala Met Asn Pro Tyr Gly Arg
145 150 155 160

Thr Lys Leu Phe Leu Glu Glu Ile Ala Arg Asp Ile Gln Lys Ala Glu
165 170 175

Pro Glu Trp Arg Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala
180 185 190

His Glu Ser Gly Ser Ile Gly Glu Asp Pro Lys Gly Ile Pro Asn Asn
195 200 205

Leu Met Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu
210 215 220

Asn Val Tyr Gly His Asp Tyr Pro Thr Glu Asp Gly Ser Ala Val Arg
225 230 235 240

Asp Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile Ala Ala Leu
245 250 255

Arg Lys Leu Phe Ala Asp Pro Lys Ile Gly Cys Thr Ala Tyr Asn Leu
260 265 270

Gly Thr Gly Gln Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu
275 280 285

Lys Ala Ser Gly Lys Lys Ile Pro Ile Lys Leu Cys Pro Arg Arg Ser
290 295 300

Gly Asp Ala Thr Ala Val Tyr Ala Ser Thr Glu Lys Ala Glu Lys Glu
305 310 315 320

Leu Gly Trp Lys Ala Lys Tyr Gly Val Asp Glu Met Cys Arg Asp Gln
325 330 335

Trp Lys Trp Ala Asn Asn Asn Pro Trp Gly Tyr Gln Asn Lys Leu
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<210> 19
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<212> PRT
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<400> 19

Met Gly Ser Ser Val Glu Gln Asn Ile Leu Val Thr Gly Gly Ala Gly
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Val	Thr	Ile	Ile	Asp	Asn	Leu	Asp	Asn	Ser	Val	Val	Glu	Ala	Val	His
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Arg	Val	Arg	Glu	Leu	Val	Gly	Pro	Asp	Leu	Ser	Thr	Lys	Leu	Glu	Phe
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Asn	Gln	Arg	Phe	Asp	Ala	Val	Ile	His	Phe	Ala	Gly	Leu	Lys	Ala	Val
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Gly	Glu	Ser	Val	Gly	Asn	Pro	Arg	Arg	Tyr	Phe	Asp	Asn	Asn	Leu	Val
			100					105					110		
Gly	Thr	Ile	Asn	Leu	Tyr	Glu	Thr	Met	Ala	Lys	Tyr	Asn	Cys	Lys	Met
		115					120					125			
Met	Val	Phe	Ser	Ser	Ser	Ala	Thr	Val	Tyr	Gly	Gln	Pro	Glu	Ile	Val
	130					135					140				
Pro	Cys	Val	Glu	Asp	Phe	Glu	Leu	Gln	Ala	Met	Asn	Pro	Tyr	Gly	Arg
145					150					155					160
Thr	Lys	Leu	Phe	Leu	Glu	Glu	Ile	Ala	Arg	Asp	Ile	His	Ala	Ala	Glu
				165					170					175	
Pro	Glu	Trp	Lys	Ile	Ile	Leu	Leu	Arg	Tyr	Phe	Asn	Pro	Val	Gly	Ala
			180					185					190		
His	Glu	Ser	Gly	Arg	Ile	Gly	Glu	Asp	Pro	Lys	Gly	Ile	Pro	Asn	Asn
		195					200					205			
Leu	Met	Pro	Tyr	Ile	Gln	Gln	Val	Ala	Val	Gly	Arg	Leu	Pro	Glu	Leu
	210					215					220				

Asn Val Phe Gly His Asp Tyr Pro Thr Met Asp Gly Ser Ala Val Arg
225 230 235 240

Asp Tyr Ile His Val Met Asp Leu Ala Asp Gly His Val Ala Ala Leu
245 250 255

Asn Lys Leu Phe Ser Asp Ser Lys Ile Gly Cys Thr Ala Tyr Asn Leu
260 265 270

Gly Thr Gly Gln Gly Thr Ser Val Leu Glu Met Val Ser Ser Phe Glu
275 280 285

Lys Ala Ser Gly Lys Lys Ile Pro Ile Lys Leu Cys Pro Arg Arg Ala
290 295 300

Gly Asp Ala Thr Ala Val Tyr Ala Ser Thr Gln Lys Ala Glu Lys Glu
305 310 315 320

Leu Gly Trp Lys Ala Lys Tyr Gly Val Asp Glu Met Cys Arg Asp Gln
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Trp Asn Trp Ala Asn Lys Asn Pro Trp Gly Phe Gln Lys Lys Pro
340 345 350

<210> 20
<211> 354
<212> PRT
<213> Cyamopsis tetragonoloba

<400> 20

Met Val Ser Ser Arg Met Ala Ser Gly Glu Thr Ile Leu Val Thr Gly
1 5 10 15

Gly Ala Gly Phe Ile Gly Ser His Thr Val Val Gln Leu Leu Lys Gln
20 25 30

Gly Phe His Val Ser Ile Ile Asp Asn Leu Tyr Asn Ser Val Ile Asp
35 40 45

Ala Val His Arg Val Arg Leu Leu Val Gly Pro Leu Leu Ser Ser Asn
 50 55 60

Leu His Phe His His Gly Asp Leu Arg Asn Ile His Asp Leu Asp Ile
 65 70 75 80

Leu Phe Ser Lys Thr Lys Phe Asp Ala Val Ile His Phe Ala Gly Leu
 85 90 95

Lys Gly Val Gly Glu Ser Val Leu Asn Pro Ser Asn Tyr Tyr Asp Asn
 100 105 110

Asn Leu Val Ala Thr Ile Asn Leu Phe Gln Val Met Ser Lys Phe Asn
 115 120 125

Cys Lys Lys Leu Val Ile Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro
 130 135 140

Asp Gln Ile Pro Cys Val Glu Asp Ser Asn Leu His Ala Met Asn Pro
 145 150 155 160

Tyr Gly Arg Ser Lys Leu Phe Val Glu Glu Val Ala Arg Asp Ile Gln
 165 170 175

Arg Ala Glu Ala Glu Trp Arg Ile Ile Leu Leu Arg Tyr Phe Asn Pro
 180 185 190

Val Gly Ala His Glu Ser Gly Gln Ile Gly Glu Asp Pro Arg Gly Leu
 195 200 205

Pro Asn Asn Leu Met Pro Tyr Ile Gln Gln Val Ala Val Ala Arg Leu
 210 215 220

Pro Glu Leu Asn Ile Tyr Gly His Asp Tyr Pro Thr Lys Asp Gly Thr
 225 230 235 240

Ala Ile Arg Asp Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile

245					250					255					
Ala	Ala	Leu	Arg	Lys	Leu	Phe	Thr	Thr	Asp	Asn	Ile	Gly	Cys	Thr	Ala
			260					265					270		
Tyr	Asn	Leu	Gly	Thr	Gly	Arg	Gly	Thr	Ser	Val	Leu	Glu	Met	Val	Ala
		275					280					285			
Ala	Phe	Glu	Lys	Ala	Ser	Gly	Lys	Lys	Ile	Pro	Ile	Lys	Met	Cys	Pro
	290					295					300				
Arg	Arg	Pro	Gly	Asp	Ala	Thr	Ala	Val	Tyr	Ala	Ser	Thr	Glu	Lys	Ala
305					310					315					320
Glu	Lys	Glu	Leu	Gly	Trp	Lys	Ala	Lys	Tyr	Gly	Val	Glu	Glu	Met	Cys
				325					330					335	
Arg	Asp	Gln	Trp	Lys	Trp	Ala	Ser	Asn	Asn	Pro	Trp	Gly	Tyr	Gln	Gly
			340					345					350		
Lys His															